

GenCore version 5.1.4_p5-4578
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ON nucleic - nucleic search, using sw model

Run on: March 11, 2003, 05:12:58 ; Search time 3016 Seconds

(without alignments)
17903.101 Million cell updates/sec

Title: US-10-046-433-39
Perfect score: 3334
Sequence: 1 gcagaaagcagcgcgcagc.....attaaaaaaaaaaaaaa 3334

Scoring table: IDENTITY_NUC
GapOp 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:

32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthun:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_eston:*

17: gb_gss:*

18: em_gss_num:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_rnt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rnd:*

ALIGNMENTS

RESULT 1

AK017241 LOCUS AK017241 DEFINITION 1773 bp mRNA linear HTC 19-JAN-2002

Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone-533017022;homolog to KIAA1324 PROTEIN (FRAGMENT), full insert sequence.

ACCESSION

AK017241

1

GI:12056379

VERSION

AK017241.1

KEYWORDS

CAP trapper.

SOURCE

Mus musculus (strain: C57BL/6J) adult male pituitary gland cDNA to mRNA, clone-11b:RIKEN full-length enriched mouse cDNA library

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1236	37.1	1773	AK017241
2	840.6	25.2	1069	BQ278843
3	705	21.1	705	BMB30016
4	675	20.2	687	BM791383
5	665	20.0	689	BM791435
6	625.2	18.8	685	AV751975
7	596.8	17.9	936	14 BQ954456
8	593.8	17.8	653	10 AW994023
9	585	17.5	609	12 BE969851
10	563.6	16.9	879	12 BF979362
11	559.2	16.8	608	14 BM790880
12	558.4	16.7	1096	12 BG245770
13	552	16.6	564	9 AI301140
14	546.4	16.4	848	13 B15622019
15	539.2	16.2	744	13 B1526944
16	539.2	16.2	1008	12 BF979911
17	538.8	16.2	731	13 BG64392
18	536.4	16.1	559	14 BQ083862
19	534	16.0	779	13 B1692291
20	527.2	15.8	849	12 BQ581951
21	525.8	15.8	930	9 AL708563
22	525.2	15.8	530	9 AL708563
23	521.8	15.7	774	13 BQ28492
24	518.2	15.5	10 BQ218431	
25	517.8	15.5	552	10 AW137691
26	515.6	15.5	797	12 BF123383
27	509	15.3	521	12 BF081676
28	507.6	15.2	529	12 BQ951260
29	503.8	15.1	611	10 BQ618558
30	498.2	14.9	555	10 AW966212
31	495.6	14.9	616	10 BB611535
32	495	14.8	516	14 BQ021096
33	492.8	14.8	507	12 BB769189
34	490.8	14.7	906	12 BF11940
35	488.4	14.6	528	12 BF744823
36	485.6	14.6	492	14 BF855444
37	485	14.5	893	12 BP535059
38	484.4	14.5	528	9 AR90726
39	481	14.4	493	9 AR89507
40	478.8	14.4	494	9 AL56507
41	477.4	14.2	862	13 BQ1081786
42	469.4	14.1	484	9 AL683933
43	468.8	14.1	497	9 AA399077
44	466.6	14.0	810	12 BF164971
45	462.4	13.9	477	9 AI923722

REFERENCE	AUTHORS	JOURNAL	TITLE	PUBLISHER
4	Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Kono,H., Adachi,J., Fukuda,S., Arizawa,M., Izawa,M., Nishi,K., Kyosawa,H., Kono,S., Yamamoto,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,R., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Hono,H., Baldarelli,R., Basch,G., Blaize,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.P., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamia,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,T., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,H., Weitz,C., Whitaker,C., Wilming,L., Wijmenga,C., Yoshiba,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Konotsuki,S., and Hayashizaki,Y.		Functional annotation of a full-length mouse cDNA collection	
5	{bases 1 to 1773}	Nature	409 (6821), 685-690 (2001)	
5	Adachi,J., Alzawa,K., Akahira,S., Akiuura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hirano,K., Hirao,T., Horii,F., Hume,D., Imori,Y., Ispili,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Kono,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,T., Okada,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,J., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sozabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Tanaka,T., Teijima,Y., Toya,T., Yamamura,T., Yamamoto,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.	Submitted (10-JUL-2000) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-resgsc@riken.go.jp, URL: http://genome.gsc.riken.go.jp/ , Tel: 81-45-503-9222, Fax: 81-45-503-9216)	Direct Submission	
6	Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.			
7	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was prepared with a primer 5' GAGAGAGAGAGGATCAAGGCCTTTRTTTTRTTTNN 3', cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap trapper. cDNA went through one round of normalization to Rot = 3.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence 5'	Submitted (10-JUL-2000) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-resgsc@riken.go.jp, URL: http://genome.gsc.riken.go.jp/ , Tel: 81-45-503-9222, Fax: 81-45-503-9216)		
8	COMMENT			

FEATURES	source	with BamHI and XbaI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FIC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.						
	ORIGIN	Location/Qualifiers						
BASE COUNT	405	a	511	c	421	9	436	t
Query Match	Best Local Similarity	37.1%	Score	1236;	DB	11;	Length	1773;
Matches	1496;	Conservative	0;	Mismatches	255;	Indels	17;	Gaps
QY	1540	GGCGAAATCAGCTTGTGCTTGAGACCTCTGGAGCTGAGCTACTTCATG	1599					
Db	1	GCCAGGATCACATGTGCTCGAGACCATCTGCTGAGACTGTGAGCTACTTCATG	60					
QY	1600	GRCGGGTGAACTCTGGACCAACACTCCCTGGAGCTGAGCTGAGCTACTTCATG	1659					
Db	61	GGGGCATGAAATCCAGGACCAATACTCTGTGGAGACGTGGAGAACGGCACAAAGGCAAG	120					
QY	1660	CACTCCATACCTACATCATGGAGGAGACACTACACGAGCTCACCTGGCCCTTCAG	1719					
Db	121	CAGTCCTATACCTACATCAAGAGAAATGCTACTCTGTGGACTTCACATGGCCCTTCAG	180					
QY	1720	AGGACCACTTTCATGAGGCAAGCAGGAAGACCTACACCATAGCTGGTGCACAGACTACTCC	1779					
Db	181	AGGACACCCTCTGAAACAGGCAGGAGTACTATGATGTCGCCAGATCTACTCA	240					
QY	1780	ATCAATGTCACCAATGTTATGATGCTGGCTG3'CTCTACTCGCGTGCCTGGCCCTTGAAGA	1839					
Db	241	ATCAATGTCACCAACGCTCATGGGGGGTGGCTCTGCACCTCTTGTCCCTGTGCCCTTGAAGA	300					
QY	1840	GCCTCTGATGTGGCTCTCTCTGCACCTCTGCTCTGCTGTGGTACTATGACCGGAGT	1899					
Db	301	GCCTCTGATGTGGCTCTCTGCACCTCTGCTCTGCTGTGGTACTATGACCGGAGT	360					
QY	1900	TCAGGAACCTGGCACTCTGCTCTGCACCTTAACAGAAATTGGAAGGCCACCGCTTATGGT	1959					
Db	361	TCTGGACCTGGCCACCTCTGTCCCTCTAACACATCTGTGAAGACGTCACCGCTTACGGT	420					
QY	1980	GTCCAGGCGCTGTTGGCCCTGGTCCAGGAGCAAGACACAGAGTCACCTCTGGC	2019					
Db	421	GCACAGGCCGCTGTTGGCCCTGGTCCAGGAGCAAGATACAGATCCACTCTCTGC	480					
QY	2020	TACATGTTGACCTCTCAGCAACACTCAACAGGAGCTTCACTACACTACTCTCC	2079					
Db	481	TACAAACGACTGTCACCTCTCCGAAACACCCAGCAGGATTTCACTACACTCTCA	540					
QY	2140	TACTTCCTACCTTGTACCTCTGCTGGAGGCCAAGCTTCACTTCAAGGTGAA	2199					
Db	601	TATTTTCATCATTCACCCCTGAGCTCTGTGGAGAACAGGGAAANAAATGCTGTGTC	660					
QY	2200	ACCGACAGTGTCACTGCACTCGGATTCAGGGTGAATGCTGGTCAATATC	2259					

Db 758 CTCGATGGACCGTGTGATGGCTGCACTTCCACTTCCGTGGAGACGGCGCTGCTG 599

Qy 2625 CCCCTCTCTCACTGGCGACTAACATCTATGTCAGCAGCTGGTGTGGCTGGATCCA 2684
Db 698 CCCCTCTCTCACTGGCGACTAACATCTATGTCAGCAGCTGGTGTGGCTGGATCCA 639Qy 2685 GAAGACTACTTACGGTGTGGAGACCCAGCTGGCTGGCGATTCCTGGCTGGATCCA 2744
Db 638 GAAGACTACTTACGGTGTGGAGACCCAGCTGGCTGGCTGGATCCA 579Qy 2745 GCAGAGAGTACCTCTGCAAACCATAGATTCTGGCTGAAGTGGGATCTGCGAG 2804
Db 578 GCAGAGAGTACCTCTGCAAACCATAGATTCTGGCTGAAGTGGGATCTGCGAG 519Qy 2805 CACCTGACTGCAACCTCTCACCGTGTGACCTGACTTCTGGCTGGCTGGATCTGCGAG 2864
Db 518 CACCTGACTGCAACCTCTCACCGTGTGACCTGACTTCTGGCTGGATCTGCGAG 459Qy 2865 ACTGAGTCAAGTACTCAAGCTGGTGTGAAGTGTACTCTAACGGACTGTGCTGCC 2924
Db 458 ACTAGATCAAGTACTCAAGCTGGTGTGAAGTGTACTCTAACGGACTGTGCTGCC 399Qy 2925 AGCGCTGACAGCTGGCCATCATGGAGAGTCAATCTTCTCCAGAGGACTCTGTATGG 2984
Db 398 AGCGCTGACAGCTGGCCATCATGGAGAGTCAATCTTCTCCAGAGGACTCTGTATGG 339Qy 2985 CAGCAGAA-TCTCTTGGAGAGTCAATCTTCTCCAGAGGACTCTGTATGG 3043
Db 338 CAGCAGAA-TCTCTTGGAGAGTCAATCTTCTCCAGAGGACTCTGTATGG 279Qy 3044 ATTTGACTGAGTGTGCGCTGAAGAGATCCAGGGGGAGACATGGACCTGTGAGGGC 3103
Db 278 ATTTGACTGAGTGTGCGCTGAAGAGATCCAGGGGGAGACATGGACCTGTGAGGGC 219Qy 3104 ACTGCTGCTCACTGCTCTCTACCTGCACTGACCTTGTGACCTTGTGAGCTGGGATT 3163
Db 218 ACTGCTGCTCACTGCTCTCTACCTGCACTGACCTTGTGAGCTGGGATT 159Qy 3164 GGGGCCAGCATCTGCAACCCACTGTGAAATCTTCACTGTGGCTTTCAGAT 3223
Db 158 GGGGCCAGCATCTGCAACCCACTGTGAAATCTTCACTGTGGCTTTCAGAT 99Qy 3224 GTTGTGATTTCAGCTTTTTAGTAGTACCAACCCCTCTCTGTGTGCTCAA 3283
Db 98 GTTGTGATTTCAGCTTTTTAGTAGTACCAACCCCTCTCTGTGTGCTCAA 39Qy 3284 CCTGCCAATATACCCACACTTGTGTAAATTA 321
Db 38 CCTGCCAATATACCCACACTTGTGTAAATTA 1

BASE COUNT

157

a

208

c

169

g

171

t

ORIGIN

Query Match

21.1%

score

705

DB

14

Length

705

Best

Local

Similarity

100.0%

Pred.

No.

2e-152

0;

Mismatches

705;

Conservative

0;

Indels

0;

Gaps

0;

Matches

705;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

Match

21.1%

score

705

DB

14

Length

705

Best

Local

Similarity

100.0%

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No.

2e-152

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Mismatches

705;

Conservative

0;

Indels

0;

Gaps

0;

Match

21.1%

score

705

DB

14

Length

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Best

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Similarity

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No.

2e-152

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Mismatches

705;

Conservative

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Indels

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Gaps

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21.1%

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Mismatches

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Conservative

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0;

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Length

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Similarity

100.0%

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No.

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Mismatches

705;

Conservative

0;

Indels

0;

Gaps

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100.0%

Pred.

No.

2e-152

0;

Mismatches

705;

Conservative

0;

Indels

0;

Gaps

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Match

21.1%

score

705

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Length

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100.0%

Pred.

No.

2e-152

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Mismatches

705;

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Length

705

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Pred.

No.

2e-152

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Mismatches

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Indels

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Gaps

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score

705

DB

14

Length

705

Best

Local

Similarity

100.0%

Pred.

No.

2e-152

0;

Mismatches

705;

Conservative

0;

Indels

0;

Gaps

0;

Match

21.1%

score

705

DB

14

Length

705

Best

Local

Similarity

100.0%

Pred.

No.

2e-152

0;

Mismatches

705;

Conservative

0;

Indels

0;

Gaps

0;

Match

21.1%

score

705

DB

14

Length

705

Best

Local

Similarity

100.0%

Pred.

No.

2e-152

0;

Mismatches

705;

Conservative

0;

Indels

0;

Gaps

0;

Match

21.1%

score

705

DB

14

Length

705

Best

Local

Similarity

100.0%

Pred.

No.

2e-152

0;

Mismatches

705;

Conservative

0;

Indels

0;

OY 2260 ACAGGCTACGCTTGCAGGAGTCATCATTCCCCCAGAGGTGAGGGCTACAGGGCGG 2319
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 Db 301 ACAGCCTACGCTTGCAGGAGTCATCATTCCCCCAGAGGTGAGGGCTACAGGGCGG 360
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 OY 2320 GTTCCCTACAGCCCTGAGCTTGCTGACTATGGG3GACACAGATGACT 2379
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 361 GTTCCCTACAGCCCTGAGCTTGCTGACTATGGG3GACACAGATGACT 420
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 OY 2380 CTGGATGGAATCACCTCCAGCAGCTGACTTACCTGGAGACACAGATGACT 2439
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 421 CTGGATGGAATCACCTCCAGCAGCTGACTTACCTGGAGACACAGATGACT 480
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 OY 2440 GTGAGCTCTTATAGGTCAGATGAGCTGACCCAGTCGAGTCGAGTCGGAGATCAC 2499
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 481 GTGAGCTCTTATAGGTCAGATGAGCTGACCCAGTCGAGTCGAGTCGGAGATCAC 540
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 OY 2500 ACCATCCGCGCTAGTGCAGTCACAGAAACCTCCCTGGAAGTTGCTGCGCCAGA 2559
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 Db 541 ACCATCCGCGCTAGTGCAGTCACAGAAACCTCCCTGGAAGTTGCTGCGCCAGA 600
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RESULT 4
 BM791383
 DEFINITION K-EST0071373 S21SNU520 Homo sapiens cDNA clone S21SNU520-14-D01 5', mRNA sequence.
 ACCESSION BM791383
 VERSION 1.1
 KEYWORDS EST.
 ORGANISM Homo sapiens
 SOURCE human.
 REFERENCE
 AUTHORS Kim, N. S., Hahn, Y., Oh, J. H., Lee, J. Y., Ann, H. Y., Chu, M. Y., Kim, M. R., Oh, K. J., Cheong, J. E., Sohn, H. Y., Kim, J. M., Park, H. S., Kim, S. and Kim, Y. S.
 TITLE JOURNAL
 COMMENT
 Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Baeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 14 row: D column: 01
 High quality sequence step: 667.
 Location/Qualifiers
 FEATURES
 Source
 1. . 687
 /organism="Homo sapiens"
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 /clone="S21SNU520-14-D01"
 /sex="F"
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 /cell_type="Floating aggregates"
 /cell_line="SNU-520"
 /lab_host="TopoIOP"
 /note="Organ: Stomach; Vector: pTZ18RPL; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand

cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60 nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okajima-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10^R by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library.

BASE COUNT 151 a 211 c 152 g 173 t
 ORIGIN
 Query Match 20.2%; Score 675; DB 14; Length 687;
 Best Local Similarity 99.9%; Pred. No. 1 8e-14;
 Matches 686; Conservative 0; Mismatches 40; Indels 1; Gaps 1;
 QY 1802 ATGGCCCTGGCCCTACTGGCGTCTGGCTGAAGCTCTGATGTTGGCTCTCTCT 1861
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 1 ATGGCCCTGGCCCTACTGGCGTCTGGCTGAAGCTCTGATGTTGGCTCTCTCT 60
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 1862 GCACCTCTGTCTGCTGGGACTATATGGACCGAGATTAGGAACCTGCGCACTCTGCC 1921
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 Db 61 GCACCTCTGTCTGCTGGGACTATATGGACCGAGATTAGGAACCTGCGCACTCTGCC 120
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 121 CCCTTAACACAACTCTGAAAGGCCACCCAGCTTATGGTGTCAGGCCCTGTCG 180
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 1982 GTCGAGGGACAAAGAACACAGATCCACTCTCTGCTCAATGATGGACCTCTCAC 2041
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 181 GTCGAGGGACAAAGAACACAGATCCACTCTCTGCTCAATGATGGACCTCTCAC 240
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 QY 2042 GCAACACTCCACCCAGGACTTCACCTACACTCTCCTGGCAAGAACGGTCACTC 2101
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 Db 241 GCAACACTCCACCCAGGACTTCACCTACACTCTCCTGGCAAGAACGGTCACTC 300
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 QY 2102 TTGCTGGAGGCCAACGTTCACTTCAAAAGCTGTGAATACTTCATCACTTACCTCA 2161
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 Db 301 TTGCTGGAGGCCAACGTTCACTTCAAAAGCTGTGAATACTTCATCACTTACCTCA 360
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 Db 361 GTCCTCTGGAAACCGGGAGGAAATGCTGTGTTGCAAGCGACAGTCACCTCC 420
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 QY 2222 GGTCTCTGGGGTGTCTCCAACTCATCACAGCCCTAGGTTGCCGTTTGGCAAC 2281
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 Db 421 GGATTCCTGGGGTGTCTCCAACTCATCACAGCCCTAGGTTGCCGTTTGGCAAC 480
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 QY 2282 TCATCATCCCCAGGGTACAGGCTACA-GGCCGGGTTCTCAGGCCGCTGAGC 2340
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 Db 481 TCATCATCCCCAGGGTACAGGCTACA-GGCCGGGTTCTCAGGCCGCTGAGC 540
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 QY 2341 CTGCGATGACTTATGGGTGACAGATGACTCTGGTGGATCACGCCCTACCTCCCA 2400
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 Db 541 CTGCGATGACTTATGGGTGACAGATGACTCTGGTGGATCACGCCCTACCTCCCA 600
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 QY 2401 GCTGAATCTTCCACCTGGCTCTGGGATACCGGAGCTGACTCTCTTATAGGCC 2460
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 Db 601 GCTGAATCTTCCACCTGGCTCTGGGATACCGGAGCTGACTCTCTTATAGGCC 660
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 QY 2461 ATGATGTGACCCAGTCTCAGTCT 2487
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RESULT 5
 BM791435
 DEFINITION K-EST0071444 S21SNU520 Homo sapiens cDNA clone S21SNU520-20-A12 5', mRNA sequence.
 ACCESSION BM791435
 VERSION 1.1 GI:1913967

KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	1. (bases 1 to 689) Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
TITLE	21C Frontier Korean EST Project 2001
JOURNAL	Unpublished (2002)
COMMENT	Contact: Kim, Y.S.
FEATURES	Gene
source	Research Center
	Korea Research Institute of Bioscience & Biotechnology
	52 Eoeun-dong Yuseong gu, Daejeon 305-333, South Korea
	fax: +82-42-860-4409
	Email: yongsang@mail.kribb.re.kr
High quality sequence	row: A
plate: 20	column: 12
Location/Qualifiers	
	1. - 689
/organism="Homo sapiens"	
/db_xref="taxon:9006"	
/clone_id="S21SN520-20-A12"	
/sex="F"	
/tissue_type="Stomach"	
/cell_type="floating aggregates"	
/cell_line="SNU-520"	
/lab_host="Top10F"	
/note="Organ: Stomach; Vector: pTZ18RPL; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECOR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The cDNA vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of ECOR I which site is also included in vector. An RNA strand converted to a DNA strand by Okazama-berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F" by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."	
BASE COUNT	151 a 211 c 154 g 173 t
ORIGIN	
Query Match	20.0%; Score 666; DB 14; Length 689;
Best Local Similarity	99.7%; Pred. No. 2.1e-143;
Matches	688; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
QY	1802 ATGGCGTGGCTCTACTCGCGTCTGCGCCAGAAGCGCTCGATGCGGCTCTCT 1861
Db	1 ATGGCGTGGCTCTACTCGCGTCTGCGCCAGAAGCGCTCGATGCGGCTCTCT 60
QY	1862 GCACCTCTGTCGCTGGTACTATATGACCGAGATCAGGAACCTGCCACTCTGCC 1921
Db	61 GCACCTCTGTCGCTGGTACTATATGACCGAGATCAGGAACCTGCCACTCTGCC 120
QY	1922 CCCCTAACACATCTGAAAGCCACCGAGCTTATGGTGTCCAGA3CCCTGTGGCTCTGTG 1981
Db	121 CCCCTAACACATCTGAAAGCCACCGAGCTTATGGTGTCCAGA3CCCTGTGGCTCTGTG 180
QY	1982 GTCCAGGGACCAAGAACACAGAACACTCTGCTGCTCAATGATGACCTCTCAC 2041
Db	181 GTCCAGGGACCAAGAACACAGAACACTCTGCTGCTCAATGATGACCTCTCAC 240
QY	2042 GCAACACTCCACCAAGGACTTCACACTCTGCTGCTCAACACGGCACTC 2101
Db	241 GCAACACTCCACCAAGGACTTCACACTCTGCTGCTCAACACGGCACTC 300
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	1. (bases 1 to 689) Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
TITLE	21C Frontier Korean EST Project 2001
JOURNAL	Unpublished (2002)
COMMENT	Contact: Kim, Y.S.
FEATURES	Gene
source	Research Center
	Korea Research Institute of Bioscience & Biotechnology
	52 Eoeun-dong Yuseong gu, Daejeon 305-333, South Korea
	fax: +82-42-860-4409
	Email: yongsang@mail.kribb.re.kr
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plate: 20	row: A
Location/Qualifiers	
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/cell_type="floating aggregates"	
/cell_line="SNU-520"	
/lab_host="Top10F"	
/note="Organ: Stomach; Vector: pTZ18RPL; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECOR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The cDNA vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of ECOR I which site is also included in vector. An RNA strand converted to a DNA strand by Okazama-berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F" by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."	
BASE COUNT	151 a 211 c 154 g 173 t
ORIGIN	
Query Match	20.0%; Score 666; DB 14; Length 689;
Best Local Similarity	99.7%; Pred. No. 2.1e-143;
Matches	688; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
QY	1802 ATGGCGTGGCTCTACTCGCGTCTGCGCCAGAAGCGCTCGATGCGGCTCTCT 1861
Db	1 ATGGCGTGGCTCTACTCGCGTCTGCGCCAGAAGCGCTCGATGCGGCTCTCT 60
QY	1862 GCACCTCTGTCGCTGGTACTATATGACCGAGATCAGGAACCTGCCACTCTGCC 1921
Db	61 GCACCTCTGTCGCTGGTACTATATGACCGAGATCAGGAACCTGCCACTCTGCC 120
QY	1922 CCCCTAACACATCTGAAAGCCACCGAGCTTATGGTGTCCAGA3CCCTGTGGCTCTGTG 1981
Db	121 CCCCTAACACATCTGAAAGCCACCGAGCTTATGGTGTCCAGA3CCCTGTGGCTCTGTG 180
QY	1982 GTCCAGGGACCAAGAACACAGAACACTCTGCTGCTCAATGATGACCTCTCAC 2041
Db	181 GTCCAGGGACCAAGAACACAGAACACTCTGCTGCTCAATGATGACCTCTCAC 240
QY	2042 GCAACACTCCACCAAGGACTTCACACTCTGCTGCTCAACACGGCACTC 2101
Db	241 GCAACACTCCACCAAGGACTTCACACTCTGCTGCTCAACACGGCACTC 300
RESULT	6
AV751975	AV751975
LOCUS	AV751975 NPD
DEFINITION	Homo sapiens cDNA clone NPD
ACCESSION	AV751975
VERSION	AV751975.1
KEYWORDS	EST.
SOURCE	Human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	1. (bases 1 to 689)
TITLE	EST.
JOURNAL	Unpublished (2000)
COMMENT	Contact: Qinghua Zhang
	Shanghai Institute of Endocrinology, Rui-Jin Hospital
	197 Rui-Jin II Road, Shanghai 200025, P. R. China
	Tel: 86-21-64370045(ex. 663332)
	Fax: 86-21-64743206
	Email: mbshlens.sitn.sh.cn
	This clone is available at Shanghai Hematology Institute in Shanghai.
	Chinese National Human Genome Center at Shanghai
	351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
FEATURES	Gene
source	Shanghai
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/tissue_type="situitary"	
/dev_stage="Adult"	
/lab_host="SOLR"	
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Query Match	18.8%; Score 625.2; DB 10; Length 689;

Best Local Similarity		Pred. No. 5.8e-134;		Matches 658; Conservative 0; Mismatches 17; Indels 5; Gaps 2;	
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120	TCTCTGTTGAAACCANGTTAGGAAATGCTGTCGACCGAAATGTCACGTCACCTCG 179				
2223	GATTCCTGAGGGTGAATGTCACGGTCTCCAAATCTATCACAGCCATACGTCAGCTGAGGT 2282				
180	GATTCCTGAGGGTGAATGTCACGGTCTCCAAATCTATCACAGCCATACGTCAGCTGAGGT 239				
2283	CATCATCCTCCCAAGGTCACGCTACAGGGGGGTTTCACAGCCCTGTCAGCT 2342				
240	CATCATCCTCCCAAGGTCACGCTACAGGGGGGTTTCACAGCCCTGTCAGCT 299				
2343	TGCTGATCGACTTATGGGTGACACAGATACTCTGATGAAATGACCTCTG 2402				
300	TGCTGATCGACTTATGGGTGACACAGATACTCTGATGAAATGACCTCTG 359				
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360	TGAACTTTCACCTGGAGTCCTGGAAATACCGACGGTATGCTGTCAGTC 419				
2463	TGATGTCACCGAGCTGTCGAGTGTGCTGTCAGGAACTGTCAGTGGCTGTGA 2522				
420	TGATGTCACCGAGCTGTCGAGTGTGCTGTCAGGAACTGTCAGTGGCTGTGA 479				
2523	ACAGAAACGCTGTCCTGGAGTGTGCTGTCAGGAACTGTCAGTGGCTGTGA 2582				
480	ACAG----CTGTCCTGGAGTGTGCTGTCAGGAACTGTCAGTGGCTGTGA 535				
2583	TGCTGTCACCTCCACTCTCTGTCGGAGGAGCGGGCTGTCAGTC 2642				
536	TGCTGTCACCTCCACTCTCTGTCGGAGGAGCGGGCTGTCAGTC 595				
2643	TGACTTACCTGGCTATGTCAGCAGCTGTCGGGGTGGATCCACAGAGACTACTTGCTGTGA 2702				
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656	GGAGGCCGCTATGCTGTGA 675				
SU LT 7					
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DEFINITION	IMAGE-0879471 NCI-CGAP_Co24	Mus musculus	CDNA clone		
SEQUENCE	B0954456				
VERSION	B0954456.1	GI:2236934			
WORDS	EST				
SYNTH	house mouse.				
ORGANISM	Mus musculus				
EBI Karvatta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
REFERENCE	1 (bases 1 to 936)				
AUTHORS	NIH-MGC	http://ncbi.nlm.nih.gov/			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
MATERIAL	Contact: Robert Strausberg, Ph.D.				
COMMENT	Email: cgbps1@mail.nih.gov				
TISSUE	Procurement: The Cepko Laboratory, Inc.				
CDNA LIBRARY	Library Arrayed by: The I.M.A.G.E. Consortium (LNL)				

QY	3050	CTCAGTGGCCGCTGAGAGCATCTTCAGGAGGCCAGATGGACCTGAGAGGACACTCC 3109
Db	721	CAGGGGCCCCGCTGAGACGCTCAGGAGGCCAGATGGACCTGAGAGGTCGCC 780
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Db	781	CG 782
RESULT 8	AW994023/	
LOCUS	AW994023	653 bp mRNA linear EST 05-JUN-2000
DEFINITION	RC3-BN036-090200-011-b10 BN0036	Homo sapiens cDNA, mRNA sequence.
ACCESSION	AW994023	
VERSION	AW994023.1	GI:8254218
KEYWORDS	EST, human.	
ORGANISM	Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1	(bases 1 to 653)
AUTHORS	Dias Neto, E., Garcia Correa, R., Veriovski-Almeida, S., Bliones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordim, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baita, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jonenewitz, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.	
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	
MEDLINE	20203663	
COMMENT	Contact: Simpson A.J.G.	
Laboratory of Cancer Genetics		
Ludwig Institute for Cancer Research		
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil		
Tel: +55-11-2704922		
Fax: +55-11-2707001		
Email: asimpson@ludwig.org.br		
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.p1?T1=&T2=RC3-BN036-090200-011-b10&t3=2002-09&t4=1)		
Seq primer: puc 18 forward		
High quality sequence start: 43		
High quality sequence stop: 652.		
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BASE COUNT	160	a 183 g 139 t
ORIGIN		
Query Match	17.8%	Score 593.8; DB 10; Length 653;
Best Local Similarity	99.3%	Pred. No. 1.1e-126;
Matches	607;	Conservative 0; Mismatches 2; Indels 2; Gaps 1;
QY	2176	CAGGGTAGGAAATGTCCTGTCGACCGAACATGCACTGACCCGGATTCCTGGAGGT 2235
Db	653	CAGGGTAGGAAATGTCCTGTCGACCGAACATGCACTGACCCGGATTCCTGGAGGT 594
QY	2236	GAGTCAGGTTCTCAAACTATCACAGCTACTCTGCGAGGAGTCATGCCCA 2295
Db	593	GAGTCAGGTTCTCAAACTATCACAGCTACTCTGCGAGGAGTCATGCCCA 534
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LOCUS	BB969851	609 bp mRNA linear EST 04-OCT-2000
DEFINITION	BB969851	NIH-MGC_78 Homo sapiens cDNA clone IMAGE:3949710 5', mRNA sequence.
ACCESSION	BB969851	
VERSION	BB969851.1	GI:10582784
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1	(bases 1 to 609)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D.	
	Email: cgsbs@mail.nih.gov	
	Tissue Procurement: CLONETECH Laboratories, Inc.	
	CDNA Library Preparation: CLONETECH Laboratories, Inc.	
	CDNA Library Arrayed by: The T.M.A.G.E. Consortium (LNLN)	
	DNA Sequencing by: Incyte Genomics, Inc.	
	Clone distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov	
	Plate: LNLN815 row: a column: 07	
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	/clone_1.lib="NIH-MGC_78"	
	/lab_host="Ph110B (T1 Phage-resistant)"	
	/note="Organ: pancreas; Vector: PDNR-LIB (Clontech);	

REFERENCE	1 (bases 1 to 879)
AUTHORS	NIH-MGC http://mgc.ncbi.nlm.nih.gov/
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.
COMMENT	Email: cgaps-r@mail.nih.gov
COMMENT	Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
COMMENT	CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and piero Carninci (RIKEN)
COMMENT	CDNA Library Arrayed by: The T.M.A.G.E. Consortium (L1NL)
COMMENT	DNA Sequencing by: Incyte Genomics, Inc.
COMMENT	Clone distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/L1NL at: http://image.l1nl.gov
COMMENT	Plate: L1AM1037 row: 9 column: 14
COMMENT	High quality sequence stop: 660.
FEATURES	1. . 879
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BASE COUNT	188
ORIGIN	a 261 c 275 g 155 t
Query Match	16.9%; Score 563.6; DB 12; Length 879;
Best Local Similarity	97.4%; Pred. No. 1e-119; 9; Indels 8; Gaps 6;
Matches	637; conservative: 0; Mismatches
QY	4 GAAAGCAGCGCCAGCACCTGAGCCCTACTGCGCCTCTACTCAGACACCGCTATGGCT 63
Db	85 GAAAGCAGCGCCAGCACCTGAGCCCTACTGCGCCTCTACTCAGACACCGCTATGGCT 144
QY	64 GAGCCCTGGGAGACGCCACCTCTCGCGCAGAGTCAGGGAGACTGAGGAGCCATA 123
Db	145 GAGCCCTGGGAGACGCCACCTCTCGCGCAGAGTCAGGGAGACTGAGGAGCCATA 204
QY	124 CCCGGCTGGGGCTGCTGCTCTGGCCTGGGAGACGCCCTCCAGGTAGCCAGAAC 183
Db	205 CCCGGCTGGGGCTGCTGCTCTGGCCTGGGAGACGCCCTCCAGGTAGCCAGAAC 263
QY	184 GGACCGGAGCTACGCCTGAGAGACTGAGTACCACTATGAGTACAGGGGTTGAC 243
Db	264 GGACCGGAGCTACGCCTGAGAGACTGAGTACCACTATGAGTACAGGGGTTGAC 323
QY	244 AGCACGGTTCAGGGTGAAGGGCACGAGTCCTCTCTGCAACGGGGGGTTCCTGGAT 303
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QY	304 CCTGACCCGTCAGGGCACGAGTCCTCTCTGCAACGGGGGGTTCCTGGAT 363
Db	384 CCTGACCCGTCAGGGCACGAGTCCTCTCTGCAACGGGGGGTTCCTGGAT 443
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QY	424 CGGTGATGAGTGGGATGAGCTG-CCCATGGCTGAGGGCCGCTACTCCCTCGCACAGGAT 483
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QY	484 CTGGATGACAGTGTGCTGAGTCACCC-GGGAAGTGTACTGTCAGTGGTTGCC 540
SUMT 10	979362
CDS	BF979362
DEFINITION	879 bp mRNA linear EST 23-JAN-2001
M	Homo sapiens
M	IMAGE:4374181 5'
ORGANISM	Mammalia; Butheria; Primates; Catarrhini; Hominoidea; Homo. human. Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominoidea; Homo.

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Qy	541	CGGGGGACTACATCCSCTTCHACCGAGGATGCACA-GCCACACTGATGTCGCGGT	599	Qy	1942	GCACCAAGCCATTATGGTGCCTCAGGGCTGTGTCAGGGACAGAAC	2001
Db	622	CGGGGGACTACATCCSCTTCHACCGAGGATGCACA-GCCACACTGATGTCGCGGT	681	Db	68	GCACCAAGCCATTATGGTGCCTCAGGGCTGTGTCAGGGACAGAAC	127
Qy	600	CAACCTGAACTATGCGCACCGTAACTCGAATACATGACTATCCAGTCAG 653		Qy	2002	AAGATCCACTCTGTGTCATAATGATGTCGACCTTCAGGCTGTGTCAGGAACTCCACAGACT	2061
Db	682	CAA-CTGAACGCAATCTGACACCGGTAACCTCGATAACTACTATCAGATCCAG	734	Db	128	AAGATCCACTCTGTGTCATAATGATGTCGACCTTCAGGCTGTGTCAGGAACTCCACAGACT	187
RESULT	11			Qy	2052	TGAACTACACTCTCGCTTGGCAAACACGGTACTCTTGCTGGAGGGCAAGCTC	2121
LOCUS	BM790880	608 bp mRNA linear EST 05-MAR-2002		Db	188	TTCACACTACACTCTCGCTTGGCAAACACGGTACTCTTGCTGGAGGGCAAGCTC	247
DEFINITION	K-EST070769	S21SN520 Homo sapiens cDNA clone S21SN520-13-A09 5', mRNA sequence.		Qy	2122	ACTCCAAAGGGTGAATACATTCACACTTACCCATGCTTGACGTCAGTCTGAGGAAACAGGT	2181
ACCESSION	BM790880			Db	248	ACTCCAAAGGGTGAATACATTCACACTTACCCATGCTTGACGTCAGTCTGAGGAAACAGGT	307
VERSION	BM790880.1	GI:19139112		Qy	2182	AGGAATAATGCTGTTGACGACATGTCACGTGACCTCCGGATTCCTGAGGGTGA 2241	
KEYWORDS	human.			Db	308	AGGAAATGCTGTTGACGACATGTCACGTGACCTCCGGATTCCTGAGGGTGA 367	
SOURCE	Homo sapiens			Qy	2242	GGGTCTCCAACTATGACGCTACGTCGCTGCGAGTCATCCCAGAGGTG	2301
ORGANISM	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			Db	368	GGGTCTCCAACTATGACGCTACGTCGCTGCGAGTCATCCCAGAGGTG	427
REFERENCE	1 (bases 1 to 608), Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Kim, N.S., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Oh, K.J.			Qy	2302	ACAGGCTACAA-GGCCGGGTTCCTCAGCCTGTCAGGCTGTGCTGATGACTA-TTG	2359
AUTHORS	BM790880			Db	428	ACAGGCTACAA-GGCCGGGTTCCTCAGCCTGTCAGGCTGTGCTGATGACTA-TTG	487
TITLE	21C Frontier Korean EST Project 2001			Qy	2360	GGGTGACAAAGATGACTCTGGTGCACGACATGTCACGTGACCTCCGGATTCCTGAGGGTGA 2419	
JOURNAL	unpublished (2002)			Db	488	GGGTGACAAAGATGACTCTGGTGCACGACATGTCACGTGACCTCCGGATTCCTGAGGGTGA 547	
COMMENT	Contact: Kim, Y.S.			Qy	2420	AGTCTTGGATA-CCGAGCTGATCTCTTTATAGTCCATGATGTCAGCCAGTC	2478
FEATURES	source			Db	548	AGTCCTTGGATAACCGGGAGGATCTCTTTATAGTCCAAATGATGTCAGCCAGTC	607
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	/note="Organ: Stomach; Vector: PT18RPL; Site: 1: ECORI; Site: 2: NotI: The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA:RNA linker including ECO RI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dr-tailed vector. The dr-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of ECO RI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F, by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."						
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 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"
 BASE COUNT 299 a 298 c 278 g 219 t 2 others
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 Qy 3048 GACTCAGTGGCGCTGAGACATCTCAGGAGGCCAGACTGGACCTGAGAGGACTG 3107

Db	264	GACTCTGTGCGCTGAAGACATCCCTCGAGGAGGCCAGACATGACCTGTGAGAGGGACT 205	Qy	61	GCTGAGCCGGCAGACGCCACCATCTCAGCCAGAGTCAAGGGAGAACTGAGAGGGCC 120
Qy	3108	CCTGCTCTACCTGCCTCCTACCTGCATASCACCTTGCAAGCCCTGCGGCGATTGGT 3167	Db	219	GCTGAGCCGGCAGACGCCACCATCTCAGCCAGAGTCAAGGGAGAACTGAGAGGGCC 278
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DEFINITION	BI562019	848 bp mRNA linear EST 05-SEP-2001	Db	399	GACAGCACGGGTTCCAGGTGAGGCTGCGCGCATACCCGGCCATGCGCACAGC 458
ACCESSION	BI562019	mRNA sequence.	Db	301	CTGCCGTGACCCGCAAGGCACCCAGCTCCCTCTGCAAGGAGTCTGAGTACACCTATGAGTACACGGCT 360
VERSION	BI562019.1	GT:15449333	Db	459	CTGCCGTGACCCGCAAGGCACCCAGCTCCCTCTGCAAGGAGTCTGAGTACACGGCT 517
SOURCE	human.		Db	361	GATATGAGGACCACTGATGAGTGGATGAGCTGGCCATACCCGGCCATGCGCACAGC 420
ORGANISM	Homo sapiens		Db	518	GATATGAGGACCACTGATGAGTGGATGAGCTGGCCATACCCGGCCATGCGCACAGC 577
REFERENCE	1	(bases 1 to 848)	Db	480	-GGACCTGGATGAGCTGGTGGTGGTCCACCGGACTGTACTCTGGTCCAGGGGCT 538
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/	Db	638	GGAGACTGGATGAGCTGGTGGTGGTCCACCGGACTGTACTCTGGTCCAGGGGCT 696
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		Db	539	CCCGGGGCACTACATCGCCTCAACACGGACGATGGCACGCCACT-GATGACGCC 597
JOURNAL	Unpublished (1999)		Db	697	CCCGGGGCACTACATCGCCTCAACACGGACGATGGCACAGGCCACT-GATGACGCC 756
COMMENT	Contact: Robert Strausberg, Ph.D.		Db	598	GTCAACCTGAGCAACTGCCACCCCTAACCTCGATACT 637
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov			Db	757	GGTCACGTGAAACATCTGGGACCGGTACATCGAAAT 796
Tissue procurement: Miklos Palkovits, M.D., Ph.D.					
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)					
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)					
DNA Sequencing by: Incyte Genomics, Inc.					
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov					
Plate: LLNL1752 row: 1 column: 18					
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Location/Qualifiers					
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DEFINITION	BI562019	mRNA sequence.	Db	219	GCTGAGCCGGCAGACGCCACCATCTCAGCCAGAGTCAAGGGAGAACTGAGAGGGCC 278
ACCESSION	BI562019		Qy	121	ATACCCCGGCTGCGGGCTGCCCTCGCGCAGGAGACTGAGAGGGCA 180
VERSION	BI562019.1	GT:15449333	Db	279	ATACCCCGGCTGCGGGCTGCCCTCGCGCAGGAGACTGAGAGGGCA 338
SOURCE	human.		Qy	181	ACGGACCGAGCTCACCCCTGCAAGAAGTCTGAGTACACCCGCT 240
ORGANISM	Homo sapiens		Db	339	ACGGACCGAGCTCACCCCTGCAAGAAGTCTGAGTACACCCGCT 398
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov			Db	459	CTGCCGTGACCCGCAAGGCACCCAGCTCCCTCTGCAAGGAGTCTGAGTACACGGCT 517
Plate: LLNL1752 row: 1 column: 18			Db	361	GATATGAGGACCACTGATGAGTGGATGAGCTGGCCATACCCGGCCATGCGCACAGC 420
High quality sequence stop: 708.			Db	518	GATATGAGGACCACTGATGAGTGGATGAGCTGGCCATACCCGGCCATGCGCACAGC 577
Location/Qualifiers			Db	578	ATTCGTTGATGAGTGGATGAGCTGGCCATACCCGGCCATGCGCACAGC 637
FEATURES	1. . 848		Db	480	-GGACCTGGATGAGCTGGTGGTGGTCCACCGGACTGTACTCTGGTCCAGGGGCT 538
source	/organism="Homo sapiens"		Db	638	GGAGACTGGATGAGCTGGTGGTGGTCCACCGGACTGTACTCTGGTCCAGGGGCT 696
	/db_xref="taxon:6606"		Db	539	CCCGGGGCACTACATCGCCTCAACACGGACGATGGCACGCCACT-GATGACGCC 597
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RESULTS	15				
RESULT 15					
LOCUS	BI526944	744 bp mRNA linear EST 29-AUG-2001	Qy	61	GCTGAGCCGGCAGACGCCACCATCTCAGCCAGAGTCAAGGGAGAACTGAGAGGGCC 120
DEFINITION	BI526944	mRNA sequence.	Db	219	GCTGAGCCGGCAGACGCCACCATCTCAGCCAGAGTCAAGGGAGAACTGAGAGGGCC 278
ACCESSION	BI526944		Qy	121	ATACCCCGGCTGCGGGCTGCCCTCGCGCAGGAGACTGAGAGGGCA 180
VERSION	BI526944.1	GT:15351735	Db	279	ATACCCCGGCTGCGGGCTGCCCTCGCGCAGGAGACTGAGAGGGCA 338
SOURCE	EST.		Qy	181	ACGGACCGAGCTCACCCCTGCAAGAAGTCTGAGTACACCCGCT 240
ORGANISM	Mus musculus		Db	339	ACGGACCGAGCTCACCCCTGCAAGAAGTCTGAGTACACCCGCT 398
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov			Db	459	CTGCCGTGACCCGCAAGGCACCCAGCTCCCTCTGCAAGGAGTCTGAGTACACGGCT 517
Plate: LLNL1751 row: 0 column: 05			Db	361	GATATGAGGACCACTGATGAGTGGATGAGCTGGCCATACCCGGCCATGCGCACAGC 420
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Location/Qualifiers			Db	578	ATTCGTTGATGAGTGGATGAGCTGGCCATACCCGGCCATGCGCACAGC 637
FEATURES	1. . 744		Db	480	-GGACCTGGATGAGCTGGTGGTGGTCCACCGGACTGTACTCTGGTCCAGGGGCT 538
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RESULTS	15				
RESULT 15					
LOCUS	BI526944	744 bp mRNA linear EST 29-AUG-2001	Qy	61	GCTGAGCCGGCAGACGCCACCATCTCAGCCAGAGTCAAGGGAGAACTGAGAGGGCC 120
DEFINITION	BI526944	mRNA sequence.	Db	219	GCTGAGCCGGCAGACGCCACCATCTCAGCCAGAGTCAAGGGAGAACTGAGAGGGCC 278
ACCESSION	BI526944		Qy	121	ATACCCCGGCTGCGGGCTGCCCTCGCGCAGGAGACTGAGAGGGCA 180
VERSION	BI526944.1	GT:15351735	Db	279	ATACCCCGGCTGCGGGCTGCCCTCGCGCAGGAGACTGAGAGGGCA 338
SOURCE	EST.		Qy	181	ACGGACCGAGCTCACCCCTGCAAGAAGTCTGAGTACACCCGCT 240
ORGANISM	Mus musculus		Db	339	ACGGACCGAGCTCACCCCTGCAAGAAGTCTGAGTACACCCGCT 398
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov			Db	459	CTGCCGTGACCCGCAAGGCACCCAGCTCCCTCTGCAAGGAGTCTGAGTACACGGCT 517
Plate: LLNL1751 row: 0 column: 05			Db	361	GATATGAGGACCACTGATGAGTGGATGAGCTGGCCATACCCGGCCATGCGCACAGC 420
High quality sequence stop: 733.			Db	518	GATATGAGGACCACTGATGAGTGGATGAGCTGGCCATACCCGGCCATGCGCACAGC 577
Location/Qualifiers			Db	578	ATTCGTTGATGAGTGGATGAGCTGGCCATACCCGGCCATGCGCACAGC 637
FEATURES	1. . 744		Db	480	-GGACCTGGATGAGCTGGTGGTGGTCCACCGGACTGTACTCTGGTCCAGGGGCT 538
source	/organism="Mus musculus"		Db	638	GGAGACTGGATGAGCTGGTGGTGGTCCACCGGACTGTACTCTGGTCCAGGGGCT 696
	/db_xref="taxon:6606"		Db	539	CCCGGGGCACTACATCGCCTCAACACGGACGATGGCACGCCACT-GATGACGCC 597
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RESULTS	15				
RESULT 15					
LOCUS	BI526944	744 bp mRNA linear EST 29-AUG-2001	Qy	61	GCTGAGCCGGCAGACGCCACCATCTCAGCCAGAGTCAAGGGAGAACTGAGAGGGCC 120
DEFINITION	BI526944	mRNA sequence.	Db	219	GCTGAGCCGGCAGACGCCACCATCTCAGCCAGAGTCAAGGGAGAACTGAGAGGGCC 278
ACCESSION	BI526944		Qy	121	ATACCCCGGCTGCGGGCTGCCCTCGCGCAGGAGACTGAGAGGGCA 180
VERSION	BI526944.1	GT:15351735	Db	279	ATACCCCGGCTGCGGGCTGCCCTCGCGCAGGAGACTGAGAGGGCA 338
SOURCE	EST.		Qy	181	ACGGACCGAGCTCACCCCTGCAAGAAGTCTGAGTACACCCGCT 240
ORGANISM	Mus musculus		Db	339	ACGGACCGAGCTCACCCCTGCAAGAAGTCTGAGTACACCCGCT 398
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov			Db	459	CTGCCGTGACCCGCAAGGCACCCAGCTCCCTCTGCAAGGAGTCTGAGTACACGGCT 517
Plate: LLNL1751 row: 0 column: 05			Db	361	GATATGAGGACCACTGATGAGTGGATGAGCTGGCCATACCCGGCCATGCGCACAGC 420
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Location/Qualifiers			Db	578	ATTCGTTGATGAGTGGATGAGCTGGCCATACCCGGCCATGCGCACAGC 637
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RESULTS	15				
RESULT 15					
LOCUS	BI526944	744 bp mRNA linear EST 29-AUG-2001	Qy	61	GCTGAGCCGGCAGACGCCACCATCTCAGCCAGAGTCAAGGGAGAACTGAGAGGGCC 120
DEFINITION	BI526944	mRNA sequence.	Db	219	GCTGAGCCGGCAGACGCCACCATCTCAGCCAGAGTCAAGGGAGAACTGAGAGGGCC 278
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VERSION	BI526944.1	GT:15351735	Db	279	ATACCCCGGCTGCGGGCTGCCCTCGCGCAGGAGACTGAGAGGGCA 338
SOURCE	EST.		Qy	181	ACGGACCGAGCTCACCCCTGCAAGAAGTCTGAGTACACCCGCT 240
ORGANISM	Mus musculus		Db	339	ACGGACCGAGCTCACCCCTGCAAGAAGTCTGAGTACACCCGCT 398
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov			Db	459	CTGCCGTGACCCGCAAGGCACCCAGCTCCCTCTGCAAGGAGTCTGAGTACACGGCT 517
Plate: LLNL1751 row: 0 column: 05			Db	361	GATATGAGGACCACTGATGAGTGGATGAGCTGGCCATACCCGGCCATGCGCACAGC 420
High quality sequence stop: 733.			Db	518	GATATGAGGACCACTGATGAGTGGATGAGCTGGCCATACCCGGCCATGCGCACAGC 577
Location/Qualifiers			Db	578	ATTCGTTGATGAGTGGATGAGCTGGCCATACCCGGCCATGCGCACAGC 637
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RESULTS	15				
RESULT 15					
LOCUS	BI526944	744 bp mRNA linear EST 29-AUG-2001	Qy	61	GCTGAGCCGGCAGACGCCACCATCTCAGCCAGAGTCAAGGGAGAACTGAGAGGGCC 120
DEFINITION	BI526944	mRNA sequence.	Db	219	GCTGAGCCGGCAGACGCCACCATCTCAGCCAGAGTCAAGGGAGAACTGAGAGGGCC 278
ACCESSION	BI526944		Qy	121	ATACCCCGGCTGCGGGCTGCCCTCGCGCAGGAGACTGAGAGGGCA 180
VERSION	BI526944.1	GT:15351735	Db	279	ATACCCCGGCTGCGGGCTGCCCTCGCGCAGGAGACTGAGAGGGCA 338
SOURCE	EST.		Qy	181	ACGGACCGAGCTCACCCCTGCAAGAAGTCTGAGTACACCCGCT 240
ORGANISM	Mus musculus		Db	339	ACGGACCGAGCTCACCCCTGCAAGAAGTCTGAGTACACCCGCT 398
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov			Db	459	CTGCCGTGACCCGCAAGGCACCCAGCTCCCTCTGCAAGGAGTCTGAGTACACGGCT 517
Plate: LLNL1751 row: 0 column: 05			Db	361	GATATGAGGACCACTGATGAGTGGATGAGCTGGCCATACCCGGCCATGCGCACAGC 420
High quality sequence stop: 733.			Db	518	GATATGAGGACCACTGATGAGTGGATGAGCTGGCCATACCCGGCCATGCGCACAGC 577
Location/Qualifiers			Db	578	ATTCGTTGATGAGTGGATGAGCTGGCCATACCCGGCCATGCGCACAGC 637
FEATURES	1. . 744		Db	480	-GGACCTGGATGAGCTGGTGGTGGTCCACCGGACTGTACTCTGGTCCAGGGGCT 538
source	/organism="Mus musculus"		Db	638	GGAGACTGGATGAGCTGGTGGTGGTCCACCGGACTGTACTCTGGTCCAGGGGCT 696
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	/lab_host="DH10B"		Db	757	GGTCACGTGAAACATCTGGGACCGGTACATCGAAAT 796
RESULTS	15				
RESULT 15					
LOCUS	BI526944	744 bp mRNA linear EST 29-AUG-2001	Qy	61	GCTGAGCCGGCAGACGCCACCATCTCAGCCAGAGTCAAGGGAGAACTGAGAGGGCC 120
DEFINITION	BI526944	mRNA sequence.	Db	219	GCTGAGCCGGCAGACGCCACCATCTCAGCCAGAGTCAAGGGAGAACTGAGAGGGCC 278
ACCESSION	BI526944		Qy	121	ATACCCCGGCTGCGGGCTGCCCTCGCGCAGGAGACTGAGAGGGCA 180
VERSION	BI526944.1	GT:15351735	Db	279	ATACCCCGGCTGCGGGCTGCCCTCGCGCAGGAGACTGAGAGGGCA 338
SOURCE	EST.		Qy	181	ACGGACCGAGCTCACCCCTGCAAGAAGTCTGAGTACACCCGCT 240
ORGANISM	Mus musculus		Db	339	ACGGACCGAGCTCACCCCTGCAAGAAGTCTGAGTACACCCGCT 398
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov			Db	459	CTGCCGTGACCCGCAAGGCACCCAGCTCCCTCTGCAAGGAGTCTGAGTACACGGCT 517
Plate: LLNL1751 row: 0 column: 05			Db	361	GATATGAGGACCACTGATGAGTGGATGAGCTGGCCATACCCGGCCATGCGCACAGC 420
High quality sequence stop: 733.			Db	518	GATATGAGGACCACTGATGAGTGGATGAGCTGGCCATACCCGGCCATGCGCACAGC 577
Location/Qualifiers			Db	578	ATTCGTTGATGAGTGGATGAGCTGGCCATACCCGGCCATGCGCACAGC 637
FEATURES	1. . 744		Db	480	-GGACCTGGATGAGCTGGTGGTGGTCCACCGGACTGTACTCTGGTCCAGGGGCT 538
source	/organism="Mus musculus"		Db	638	GGAGACTGGATGAGCTGGTGGTGGTCCACCGGACTGTACTCTGGTCCAGGGGCT 696
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	/lab_host="DH10B"		Db	757	GGTCACGTGAAACATCTGGGACCGGTACATCGAAAT 796

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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

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BASE COUNT	ORIGIN	162 a	227 c	172 g	183 t
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				Indels	3;
				Gaps	2;
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Db	1	ACTAAATGATGTCGCCAGATCTACTCAATGTCACCAATGTCACCGGTGCA			60
Qy	1813	TCTACTGCGCTCCCTGTCGCCAGAGCTCTGATGTCAGTGGCTCCTCTGCACCTCTGT			1872
Db	61	TCTACTGCGCTCCCTGTCGCCAGAGCTCTGATGTCAGTGGCTCCTCTGCACCTCTGT			120
Qy	1873	CCTGCCTGGTAACTATATTGACCCAGATTAGGAACCTGCGCACTCTGCCACCTAACACA			1932
Db	121	CTCTGCTGCCATACATCAACCGGATCTGGACCTCTGCCACCTCTGCCCCCTAACACC			180
Qy	1933	ATTCCTGAAAGCCACAGCCTTGTGTCAGGCTTAAGTGGTGTGCAAGGCTGTGTCAGGGACC			1992
Db	181	ATCCCTGAAAGCTTACCGCTTACGGCTTACGGTGCACAGGCTGTGTCAGGGTCCA-GGACC			239
Qy	1993	ANGACACAACAGATCCACCTCTGCTACATGATGACCTGACCCCTCTCACGCCAACACTCA			2052
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Qy	2053	ACCAAGACTTCTCACTACACTCTCCTCCGCCTTGCACAAACACCC3TCACCTCTGCTGGAGGG			2112
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Qy	2113	CCAACCTTCACTCTCAAAGGTTGAAATACTTCATCATCTTACCTTACCCCTCAGTCCTCTGTGA			2172
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Qy	2173	AACCAAGGTTAGGAATAATGCTGTCACCGAACATGTCACCTACCC			2232
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Qy	2233	GGTGAGTCAGGGTCTCCAAATCTATCAGACGCCATACGTCAGGCGACTCATCCC			2292
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Qy	2293	CCAGAGGTGACAGCTACAGAGGGGTTCTCACGCCCTCTCACGCCCTCTGTGACGGA			2352
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Qy	2473	CAGCTGAGTCCTGGGAGTCAC			2498
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Search completed: March 11, 2003, 08:12:41

Job time : 3049 secs

